



1/16

#4

SEQUENCE LISTING

<110> Huang, Qian
Richmond, Joan F.L.
Cho, Bryan K.
Palliser, Deborah
Chen, Jianzhu
Eisen, Herman N.
Young, Richard A.

<120> In Vivo CTL Elicitation By Heat Shock
Protein Fusion Proteins Maps To A Discrete Domain and is
CD4+T Cell-Independent

<130> 0399.2006-003

<140> US 09/761,534

<141> 2001-01-16

<150> PCT/US00/32831

<151> 2000-12-01

<150> US 60/176,143

<151> 2000-01-14

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 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
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 tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt gag gtg 144
 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
 35 40 45
 ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc gat cgc 192
 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
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 acc gtg cgc tcg gtc aag cga cac atg ggc agc gac tgg tcc ata gag 240
 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
 65 70 75 80

att gac ggc aag aaa tac acc gcg ccg gag atc agc gcc cgc att ctg	288
Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu	
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atg aag ctg aag cgc gac gcc gag gcc tac ctc ggt gag gac att acc	336
Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr	
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gac gcg gtt atc acg acg ccc gcc tac ttc aat gac gcc cag cgt cag	384
Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln	
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Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly	
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Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe	
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gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc cgt gcc	576
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Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro	
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tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag	816
Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln	
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ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc	864
Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg	
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Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr	
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Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln	
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Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile	
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Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
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Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
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Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
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Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
225          230          235          240
Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
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Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
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Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
275          280          285
Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
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Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
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Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
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Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
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Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
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Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn	
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Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln	
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 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
 50 55 60
 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
 65 70 75 80
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
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 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
 100 105 110
 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
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 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
 130 135 140
 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 145 150 155 160
 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
 165 170 175
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 cag ggc aac cgc acg acc ccc agc tac gtg gcc ttc acc gac acc gag 144
 Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe Thr Asp Thr Glu
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Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Leu Asn Pro Gln	
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aac acc gtg ttc gac gcg aag cgg ctg atc ggc cgc aag ttc ggc gat	240
Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Lys Phe Gly Asp	
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Ala Val Val Gln Ser Asp Met Lys His Trp Pro Phe Gln Val Val Asn	
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gac ggc gac aag ccc aag gtg cag gtg aac tac aag ggc gag agc cgg	336
Asp Gly Asp Lys Pro Lys Val Gln Val Asn Tyr Lys Gly Glu Ser Arg	
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Ser Phe Phe Pro Glu Glu Ile Ser Ser Met Val Leu Thr Lys Met Lys	
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Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp	
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Ala Gly Val Ile Ala Gly Leu Asn Val Leu Arg Ile Ile Asn Glu Pro	
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Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu	
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Asp Asn Gln Pro Gly Val Leu Ile Gln Val Tyr Glu Gly Glu Arg Ala	
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Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly	
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Lys Leu Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu	
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Val His Lys Arg Glu Glu Leu Glu Arg Val Cys Ser Pro Ile Ile Ser	
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 Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Leu Asn Pro Gln
 50 55 60

Asn	Thr	Val	Phe	Asp	Ala	Lys	Arg	Leu	Ile	Gly	Arg	Lys	Phe	Gly	Asp
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225					230					235					240
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	370					375					380				
Ser	Glu	Asn	Val	Gln	Asp	Leu	Leu	Leu	Leu	Asp	Val	Ala	Pro	Leu	Ser
385					390					395					400
Leu	Gly	Leu	Glu	Thr	Ala	Gly	Gly	Val	Met	Thr	Ala	Leu	Ile	Lys	Arg
				405					410					415	
Asn	Ser	Thr	Ile	Pro	Thr	Lys	Gln	Thr	Gln	Thr	Phe	Thr	Thr	Tyr	Ser
			420					425					430		
Asp	Asn	Gln	Pro	Gly	Val	Leu	Ile	Gln	Val	Tyr	Glu	Gly	Glu	Arg	Ala
		435					440					445			
Met	Thr	Arg	Asp	Asn	Asn	Leu	Leu	Gly	Arg	Phe	Glu	Leu	Ser	Gly	Ile
	450					455					460				
Pro	Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile
465					470					475					480
Asp	Ala	Asn	Gly	Ile	Leu	Asn	Val	Thr	Ala	Thr	Asp	Lys	Ser	Thr	Gly
				485					490					495	
Lys	Ala	Asn	Lys	Ile	Thr	Ile	Thr	Asn	Asp	Lys	Gly	Arg	Leu	Ser	Lys
			500					505					510		
Glu	Glu	Ile	Glu	Arg	Met	Val	Gln	Glu	Ala	Glu	Arg	Tyr	Lys	Ala	Glu
		515					520						525		

Asp Glu Val Gln Arg Asp Arg Val Ala Ala Lys Asn Ala Leu Glu Ser
 530 535 540
 Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly
 545 550 555 560
 Lys Leu Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu
 565 570 575
 Val Ile Ser Trp Leu Asp Ser Asn Thr Leu Ala Asp Lys Glu Glu Phe
 580 585 590
 Val His Lys Arg Glu Glu Leu Glu Arg Val Cys Ser Pro Ile Ile Ser
 595 600 605
 Gly Leu Tyr Gln Gly Ala Gly Ala Pro Gly Ala Gly Gly Phe Gly Ala
 610 615 620
 Gln Ala Pro Pro Lys Gly Ala Ser Gly Ser Gly Pro Thr Ile Glu Glu
 625 630 635 640
 Val Asp

<210> 11
 <211> 627
 <212> DNA
 <213> Unknown

<220>
 <223> Murine hsp70 -Segment II
 <221> CDS
 <222> (0)...(627)
 <223> Murine hsp70 -Segment II

<400> 11
 aag ggc gag cgc aac gtg ctc atc ttc gac ctg ggg ggc ggc acg ttc 48
 Lys Gly Glu Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe
 1 5 10 15
 gac gtg tcc atc ctg acg atc gac gac ggc atc ttc gag gtg aag gcc 96
 Asp Val Ser Ile Leu Thr Ile Asp Asp Gly Ile Phe Glu Val Lys Ala
 20 25 30
 acg gcg ggc gac acg cac ctg gga ggg gag gac ttc gac aac cgg ctg 144
 Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu
 35 40 45
 gtg agc cac ttc gtg gag gag ttc aag agg aag cac aag aag gac atc 192
 Val Ser His Phe Val Glu Glu Phe Lys Arg Lys His Lys Lys Asp Ile
 50 55 60
 agc cag aac aag cgc gcg gtg cgg cgg ctg cgc acg gcg tgt gag agg 240
 Ser Gln Asn Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu Arg
 65 70 75 80
 gcc aag agg acg ctg tcg tcc agc acc cag gcc agc ctg gag atc gac 288
 Ala Lys Arg Thr Leu Ser Ser Ser Thr Gln Ala Ser Leu Glu Ile Asp
 85 90 95
 tct ctg ttc gag ggc atc gac ttc tac aca tcc atc acg cgg gcg cgg 336
 Ser Leu Phe Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg
 100 105 110

ttc gaa gag ctg tgc tcg gac ctg ttc cgc ggc acg ctg gag ccc gtg	384
Phe Glu Glu Leu Cys Ser Asp Leu Phe Arg Gly Thr Leu Glu Pro Val	
115 120 125	
gag aag gcc ctg cgc gac gcc aag atg gac aag gcc cag atc cac gac	432
Glu Lys Ala Leu Arg Asp Ala Lys Met Asp Lys Ala Gln Ile His Asp	
130 135 140	
ctg gtg ctg gtg ggc ggc tcg acg cgc atc ccc aag gtg cag aag ctg	480
Leu Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys Val Gln Lys Leu	
145 150 155 160	
ctg cag gac ttc ttc aac ggg cgc gac ctg aac aag agc atc aac ccg	528
Leu Gln Asp Phe Phe Asn Gly Arg Asp Leu Asn Lys Ser Ile Asn Pro	
165 170 175	
gac gag gcg gtg gcc tac ggg gcg gcg gtg cag gcg gcc atc ctg atg	576
Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Ile Leu Met	
180 185 190	
ggg gac aag tcg gag aac gtg cag gac ctg ctg ctg ctg gac gtg gcg	624
Gly Asp Lys Ser Glu Asn Val Gln Asp Leu Leu Leu Leu Asp Val Ala	
195 200 205	
ccc	627
Pro	

<210> 12
 <211> 209
 <212> PRT
 <213> Unknown

<220>
 <223> Murine hsp70 - Segment II

<400> 12	
Lys Gly Glu Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe	
1 5 10 15	
Asp Val Ser Ile Leu Thr Ile Asp Asp Gly Ile Phe Glu Val Lys Ala	
20 25 30	
Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu	
35 40 45	
Val Ser His Phe Val Glu Glu Phe Lys Arg Lys His Lys Lys Asp Ile	
50 55 60	
Ser Gln Asn Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu Arg	
65 70 75 80	
Ala Lys Arg Thr Leu Ser Ser Ser Thr Gln Ala Ser Leu Glu Ile Asp	
85 90 95	
Ser Leu Phe Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg	
100 105 110	
Phe Glu Glu Leu Cys Ser Asp Leu Phe Arg Gly Thr Leu Glu Pro Val	
115 120 125	
Glu Lys Ala Leu Arg Asp Ala Lys Met Asp Lys Ala Gln Ile His Asp	
130 135 140	
Leu Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys Val Gln Lys Leu	
145 150 155 160	

Leu	Gln	Asp	Phe	Phe	Asn	Gly	Arg	Asp	Leu	Asn	Lys	Ser	Ile	Asn	Pro
				165					170					175	
Asp	Glu	Ala	Val	Ala	Tyr	Gly	Ala	Ala	Val	Gln	Ala	Ala	Ile	Leu	Met
			180					185					190		
Gly	Asp	Lys	Ser	Glu	Asn	Val	Gln	Asp	Leu	Leu	Leu	Leu	Asp	Val	Ala
		195					200					205			

Pro

<210> 13
 <211> 47
 <212> DNA
 <213> Unknown

<220>
 <223> PCR Primer

<400> 13
 gcagtactca tatgatcctg gagcttccat ttgccagtgg gacaatg 47

<210> 14
 <211> 63
 <212> DNA
 <213> Unknown

<220>
 <223> PCR Primer

<400> 14
 ctccgacctc acctacgacg ttcgcagaga cttcttaaaa ttatccgata gcctagacct 60
 agt 63

<210> 15
 <211> 44
 <212> DNA
 <213> Unknown

<220>
 <223> PCR Primer

<400> 15
 atagtactgg atccatggct cgtgcggtcg ggatcgacct cggg 44

<210> 16
 <211> 36
 <212> DNA
 <213> Unknown

<400> 16
 ggaattccta tctagtcact tgccctcccg gccgtc 36

<210> 17
 <211> 49
 <212> DNA
 <213> Unknown

<220>
<223> PCR Primer

<400> 17
gtcgacgaat tcatcatcag attcgctgct cttctcgcc cttgtcgag 49

<210> 18
<211> 48
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 18
gtcgacggat ccatggagaa ggagcagcga atcctgggtct tcgacttg 48

<210> 19
<211> 48
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 19
gtcgacggat ccatggtgaa agacgttctg ctgcttgatg ttaccccg 48

<210> 20
<211> 48
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 20
gtcgacggat ccatgcgtaa tcaagccgag acattgggtct accagacg 48

<210> 21
<211> 49
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 21
gtcgacgaat tcatcacggg gtaacatcaa gcagcagaac gtctttcac 49

<210> 22
<211> 49
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 22
gtcgacgaat tcatcagacc aatgtctcgg cttgattacg aacatcggc 49

<210> 23
<211> 33
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 23
tctagaggat ccatggccaa gaacacggcg atc 33

<210> 24
<211> 39
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 24
tctagagaat tcctaattcca cctcctcgat ggtgggtcc 39

<210> 25
<211> 24
<212> PRT
<213> Unknown

<220>
<223> P1 Peptide

<400> 25
Ile Lys Val Ser Gly Leu Glu Gln Leu Glu Ser Ile Tyr Arg Tyr Tyr
1 5 10 15
Gly Leu Leu Leu Lys Glu Ala Tyr
20